

# RAW SEQUENCE LISTING

EFS

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/649,413A

Source: 1FW16

Date Processed by STIC: 4/4/07

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IFW16

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/649,413A

DATE: 04/04/2007

TIME: 14:56:24

Input Set : N:\efs\04\_04\_07\10649413A\_efs\224160\_ST25\_2.txt  
 Output Set: N:\CRF4\04042007\J649413A.raw

4 <110> APPLICANT: Ullrich, Axel  
 5       Bange, Johannes  
 6       Knyazev, Pjotr  
 8 <120> TITLE OF INVENTION: Use of inhibitors for the treatment of RTK-hyperfunction-induced  
 9       disorders, particularly cancer  
 11 <130> FILE REFERENCE: 205884  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/649,413A  
 C--> 14 <141> CURRENT FILING DATE: 2003-08-27  
 16 <150> PRIOR APPLICATION NUMBER: PCT/EP99/00405  
 17 <151> PRIOR FILING DATE: 1999-01-22  
 19 <150> PRIOR APPLICATION NUMBER: DE 198 02 377.4  
 20 <151> PRIOR FILING DATE: 1998-01-22  
 22 <160> NUMBER OF SEQ ID NOS: 9  
 24 <170> SOFTWARE: PatentIn Ver. 3.4  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 25  
 28 <212> TYPE: PRT  
 29 <213> ORGANISM: Homo sapiens  
 31 <220> FEATURE:  
 32 <221> NAME/KEY: DOMAIN  
 33 <222> LOCATION: (1)..(25)  
 34 <223> OTHER INFORMATION: amino acid sequence of  
 35       FGFR-4 (mutant) between positions 366-390  
 37 <400> SEQUENCE: 1  
 38 Arg Tyr Thr Asp Ile Ile Leu Tyr Ala Ser Gly Ser Leu Ala Leu Ala  
 39     1               5               10               15  
 41 Val Leu Leu Leu Leu Ala Arg Leu Tyr  
 42     20              25  
 44 <210> SEQ ID NO: 2  
 45 <211> LENGTH: 25  
 46 <212> TYPE: PRT  
 47 <213> ORGANISM: Homo sapiens  
 49 <220> FEATURE:  
 50 <221> NAME/KEY: DOMAIN  
 51 <222> LOCATION: (1)..(25)  
 52 <223> OTHER INFORMATION: amino acid sequence of  
 53       FGFR-4 (wild-type) between positions 366-390  
 55 <400> SEQUENCE: 2  
 56 Arg Tyr Thr Asp Ile Ile Leu Tyr Ala Ser Gly Ser Leu Ala Leu Ala  
 57     1               5               10               15  
 59 Val Leu Leu Leu Leu Ala Gly Leu Tyr  
 60     20              25  
 62 <210> SEQ ID NO: 3

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63 <211> LENGTH: 29
64 <212> TYPE: DNA
65 <213> ORGANISM: artificial sequence
67 <220> FEATURE:
68 <223> OTHER INFORMATION: PCR primer for the amplification of FGFR-4 (wild-type and
mutant)
70 <400> SEQUENCE: 3
71 gctcagaggg cgggggggg tgccggccg 29
73 <210> SEQ ID NO: 4
74 <211> LENGTH: 33
75 <212> TYPE: DNA
76 <213> ORGANISM: artificial sequence
78 <220> FEATURE:
79 <223> OTHER INFORMATION: PCR primer for the amplification of FGFR-4 (wild-type and
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82 ccgcgtcgagt gcctgcacag ccttggcct tgc 33
84 <210> SEQ ID NO: 5
85 <211> LENGTH: 24
86 <212> TYPE: DNA
87 <213> ORGANISM: artificial sequence
89 <220> FEATURE:
90 <223> OTHER INFORMATION: PCR primer for the amplification of the transmembrane domain
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91 (wild-type and mutant)
93 <400> SEQUENCE: 5
94 gaccgcagca gcgcgcagg ccag 24
96 <210> SEQ ID NO: 6
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98 <212> TYPE: DNA
99 <213> ORGANISM: artificial sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION: PCR primer for the amplification of the transmembrane domain
of FGFR-4
103 (wild-type and mutant)
105 <400> SEQUENCE: 6
106 agagggaaaga gggagagctt ctg 23
108 <210> SEQ ID NO: 7
109 <211> LENGTH: 28
110 <212> TYPE: DNA
111 <213> ORGANISM: artificial sequence
113 <220> FEATURE:
114 <223> OTHER INFORMATION: primer for sequencing of the transmembrane domain of FGFR-4
115 (wild-type and mutant)
117 <400> SEQUENCE: 7
118 ggaaattcga ccgcgcgcgc gcccgggg 28
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121 <211> LENGTH: 25
122 <212> TYPE: DNA
123 <213> ORGANISM: artificial sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: primer for sequencing of the transmembrane domain of FGFR-4
127 (wild-type and mutant)

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129 <400> SEQUENCE: 8  
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 133 <210> SEQ ID NO: 9  
 134 <211> LENGTH: 802  
 135 <212> TYPE: PRT  
 136 <213> ORGANISM: Homo sapiens  
 138 <400> SEQUENCE: 9  
 140 Met Arg Leu Leu Leu Ala Leu Leu Gly Val Leu Leu Ser Val Pro Gly  
 141 1 5 10 15  
 144 Pro Pro Val Leu Ser Leu Glu Ala Ser Glu Glu Val Glu Leu Glu Pro  
 145 20 25 30  
 148 Cys Leu Ala Pro Ser Leu Glu Gln Gln Glu Gln Glu Leu Thr Val Ala  
 149 35 40 45  
 152 Leu Gly Gln Pro Val Arg Leu Cys Cys Gly Arg Ala Glu Arg Gly Gly  
 153 50 55 60  
 156 His Trp Tyr Lys Glu Gly Ser Arg Leu Ala Pro Ala Gly Arg Val Arg  
 157 65 70 75 80  
 160 Gly Trp Arg Gly Arg Leu Glu Ile Ala Ser Phe Leu Pro Glu Asp Ala  
 161 85 90 95  
 164 Gly Arg Tyr Leu Cys Leu Ala Arg Gly Ser Met Ile Val Leu Gln Asn  
 165 100 105 110  
 168 Leu Thr Leu Ile Thr Gly Asp Ser Leu Thr Ser Ser Asn Asp Asp Glu  
 169 115 120 125  
 172 Asp Pro Lys Ser His Arg Asp Pro Ser Asn Arg His Ser Tyr Pro Gln  
 173 130 135 140  
 176 Gln Ala Pro Tyr Trp Thr His Pro Gln Arg Met Glu Lys Lys Leu His  
 177 145 150 155 160  
 180 Ala Val Pro Ala Gly Asn Thr Val Lys Phe Arg Cys Pro Ala Ala Gly  
 181 165 170 175  
 184 Asn Pro Thr Pro Thr Ile Arg Trp Leu Lys Asp Gly Gln Ala Phe His  
 185 180 185 190  
 188 Gly Glu Asn Arg Ile Gly Gly Ile Arg Leu Arg His Gln His Trp Ser  
 189 195 200 205  
 192 Leu Val Met Glu Ser Val Val Pro Ser Asp Arg Gly Thr Tyr Thr Cys  
 193 210 215 220  
 196 Leu Val Glu Asn Ala Val Gly Ser Ile Arg Tyr Asn Tyr Leu Leu Asp  
 197 225 230 235 240  
 200 Val Leu Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly Leu Pro  
 201 245 250 255  
 204 Ala Asn Thr Thr Ala Val Val Gly Ser Asp Val Glu Leu Leu Cys Lys  
 205 260 265 270  
 208 Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Leu Lys His Ile Val  
 209 275 280 285  
 212 Ile Asn Gly Ser Ser Phe Gly Ala Val Gly Phe Pro Tyr Val Gln Val  
 213 290 295 300  
 216 Leu Lys Thr Ala Asp Ile Asn Ser Ser Glu Val Glu Val Leu Tyr Leu  
 217 305 310 315 320  
 220 Arg Asn Val Ser Ala Glu Asp Ala Gly Glu Tyr Thr Cys Leu Ala Gly  
 221 325 330 335

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224 Asn Ser Ile Gly Leu Ser Tyr Gln Ser Ala Trp Leu Thr Val Leu Pro  
 225 340 345 350  
 228 Glu Glu Asp Pro Thr Trp Thr Ala Ala Ala Pro Glu Ala Arg Tyr Thr  
 229 355 360 365  
 232 Asp Ile Ile Leu Tyr Ala Ser Gly Ser Leu Ala Leu Ala Val Leu Leu  
 233 370 375 380  
 236 Leu Leu Ala Gly Leu Tyr Arg Gly Gln Ala Leu His Gly Arg His Pro  
 237 385 390 395 400  
 240 Arg Pro Pro Ala Thr Val Gln Lys Leu Ser Arg Phe Pro Leu Ala Arg  
 241 405 410 415  
 244 Gln Phe Ser Leu Glu Ser Gly Ser Ser Gly Lys Ser Ser Ser Leu  
 245 420 425 430  
 248 Val Arg Gly Val Arg Leu Ser Ser Ser Gly Pro Ala Leu Leu Ala Gly  
 249 435 440 445  
 252 Leu Val Ser Leu Asp Leu Pro Leu Asp Pro Leu Trp Glu Phe Pro Arg  
 253 450 455 460  
 256 Asp Arg Leu Val Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln  
 257 465 470 475 480  
 260 Val Val Arg Ala Glu Ala Phe Gly Met Asp Pro Ala Arg Pro Asp Gln  
 261 485 490 495  
 264 Ala Ser Thr Val Ala Val Lys Met Leu Lys Asp Asn Ala Ser Asp Lys  
 265 500 505 510  
 268 Asp Leu Ala Asp Leu Val Ser Glu Met Glu Val Met Lys Leu Ile Gly  
 269 515 520 525  
 272 Arg His Lys Asn Ile Ile Asn Leu Leu Gly Val Cys Thr Gln Glu Gly  
 273 530 535 540  
 276 Pro Leu Tyr Val Ile Val Glu Cys Ala Ala Lys Gly Asn Leu Arg Glu  
 277 545 550 555 560  
 280 Phe Leu Arg Ala Arg Arg Pro Pro Gly Pro Asp Leu Ser Pro Asp Gly  
 281 565 570 575  
 284 Pro Arg Ser Ser Glu Gly Pro Leu Ser Phe Pro Val Leu Val Ser Cys  
 285 580 585 590  
 288 Ala Tyr Gln Val Ala Arg Gly Met Gln Tyr Leu Glu Ser Arg Lys Cys  
 289 595 600 605  
 292 Ile His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asp Asn  
 293 610 615 620  
 296 Val Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Gly Val His His Ile  
 297 625 630 635 640  
 300 Asp Tyr Tyr Lys Lys Thr Ser Asn Gly Arg Leu Pro Val Lys Trp Met  
 301 645 650 655  
 304 Ala Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val  
 305 660 665 670  
 308 Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly Ser  
 309 675 680 685  
 312 Pro Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe Ser Leu Leu Arg Glu  
 313 690 695 700  
 316 Gly His Arg Met Asp Arg Pro Pro His Cys Pro Pro Glu Leu Tyr Gly  
 317 705 710 715 720  
 320 Leu Met Arg Glu Cys Trp His Ala Ala Pro Ser Gln Arg Pro Thr Phe

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321	725	730	735
324	Lys Gln Leu Val Glu Ala Leu Asp Lys Val Leu Leu Ala Val Ser Glu		
325	740	745	750
328	Glu Tyr Leu Asp Leu Arg Leu Thr Phe Gly Pro Tyr Ser Pro Ser Gly		
329	755	760	765
332	Gly Asp Ala Ser Ser Thr Cys Ser Ser Ser Asp Ser Val Phe Ser His		
333	770	775	780
336	Asp Pro Leu Pro Leu Gly Ser Ser Ser Phe Pro Phe Gly Ser Gly Val		
337	785	790	795
340	Gln Thr		800

**VERIFICATION SUMMARY**

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date